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A Study of Phenotype Selection Pressures on Grove Snails populations in Pulpit Wood Reserve, near Monks Riseborough.

Our research experiment on snails was designed to examine the relative importance of the evolutionary processes underlying the polymorphism of the species Cepaea nemoralis, the Grove Snail. Snails are slow animals therefore polymorphism can be viewed over a smaller geographical location. “The shell of C. nemoralis is polymorphic for colour and for the presence, number, and appearance of up to five dark bands” (Jones et al. 2009). This lead to our samples being carried out both nearby and far apart to try and isolate selection processes (gene flow, selection, drift and mutation) and examine their effects. Jones’ study of the polymorphism of Grove Snails found that those in woodland habitats mainly had pink and brown shells with few or no bands, and those found in grassy habitats predominantly had yellow banded shells, but as he suggests polymorphism is not governed by one single process and each population requires a separate explanation. Our research distinguished between the three major shell colours of the C. Nemoralis, pink, brown and yellow as well as the number of bands present. Dead snails’ shells were also sampled as shell colour or band decoration doesn’t change with morbidity. The aim of our report was to determine whether selection processes dependant on habitat influenced snail shell appearance polymorphism, and if so what the causes for these were.

Null hypothesis: There is no difference in relative frequencies of phenotypes between habitats in the populations of C. Nemoralis (Grove Snail)  
Alternative hypothesis: There is a difference in relative frequencies of phenotypes between habitats in the populations of C. Nemoralis (Grove Snail)

3 sampling locations were chosen in Pulpit Wood Reserve, near Monks Riseborough, separated by a distance of 100m at least, each within an area of 20 meters squared. This will enable us to analyse genetic drift and selection in the absence of gene flow. A sample was carried out in a grassy area at each of the 3 locations in order to increase repeating power and sampling validity, followed by a wooded area at the same location 20 meters away. The team collected samples at the same time to reduce sampling variation. 179 samples were taken in total.

After collecting all 179 samples and placing them in a table it became clear that our results greatly differed to those Jones et al found in his study. The samples taken from woodland areas were dominated by yellow shell colouring whereas the grassy areas mainly had snails with a pink shell colouring. This differs greatly to Jones’ sampling, which found the opposite of woodland areas being dominated by snails with yellow shell colouring and grassy areas dominated by pink and brown snails. There was also a wide phenotypic variation between the bands of colouring found on the snails, and samples where found with 0,1, 3 and 5 bands on their shells at each location. The most frequent band phenotype found in the grassy areas was 3-banded shells closely followed by 5-banded shells, whereas 5-banded shells dominated woodland areas.

Figure 1: This graph shows the relative frequencies of the three main shell colours of the Grove Snail in 3 different locations in Pulpit Wood Reserve. Series 1 are all samples taken from grassy areas and series 2 are all samples taken from woodland areas.

After examining the data collected a chi-squared statistical test was carried out to test our sampling results against our hypotheses. I carried out the chi- squared test on each phenotype allele separately.

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| --- | --- | --- | --- |
| Phenotype Tested | Chi- squared test Score: | 95% probability Level Figure: | Null hypothesis rejected? |
| Shell Colour | 7.13 | 9.49 | No |
| Number of Shell Bands | 12.18 | 12.59 | No |

Figure 2: A table to show the chi-squared test results of for snails sample in Pulpit Wood Reserve for both colour and number of bands on their shell.

As the table shows the chi- squared values for both Shell colour and number of bands on a shell are less than the level of significance so null hypothesis must be accepted, stating that there is no difference in relative frequencies of phenotypes between habitats in the populations of C. Nemoralis, in locations sampled at Pulpit Wood Reserve.

Accepting the null hypothesis therefore indicates that gene flow is not a highly influential selection process acting on these populations, as there are few (if any) similar patterns in allele frequencies between the isolated groups, as indicated by the chi-squared results. Furthermore, the proportions of phenotype frequencies also vary greatly between each sample replication within each habitat type, indicating that sample replications within each habitat type are not all being acted upon by the same selection pressure. This therefore eliminates natural selection as the main process causing the phenotypic variation, which indicates that the colour of a snail shell, of the number of bands it has on it, is not more or less advantageous than another shell colour or band frequency (mutation selection pressure). The range of phenotypes found was also relatively narrow, with the shells with 3 or 5 bands having a much higher frequency than other numbers of bands such as 1 or un-banded shells, which were rarely found. This was reflected in the shell colour results, which were dominated by yellow shells in the woodland areas and pink shells in the grassy areas. When there is little genetic variation, and population sample are dominated by one or two phenotypes, as I have just described in our results, genetic drift can be assumed to be a predominant selection pressure.

In conclusion, as neither gene flow, selection or mutation are significantly acting on our sampling population, and with the lack of genetic variation in the phenotype frequencies, I believe that genetic drift is the predominant selection pressure acting upon our snail sample populations in Pulpit Wood Reserve. Genetic drift is a random process whereby; certain individuals by chance leave behind more descendants than other individuals, and therefore pass on specific genes more frequently. This process acts upon all populations, but however in the absence of selection or gene flow it is the main selection process causing the observed gene frequencies in sampling populations.

References:

Jones et al. (1977). Polymorphism in Cepaea: A Problem with Too Many Solutions?. Annual Review of Ecology and Systematics. 8 (1), 109-143.